FIGURE 1

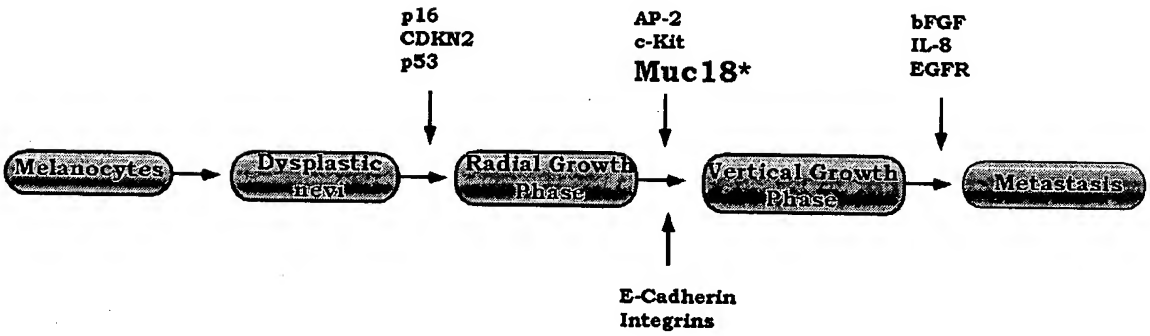
p16
CDKN2
p53
AP-2
c-Kit
Muc18*
bFGF
IL-8
EGFR
Melanocytes
Dysplastic nevi
Radial Growth Phase
Vertical Growth Phase
Metastasis
E-Cadherin
Integrins

FIGURE 2

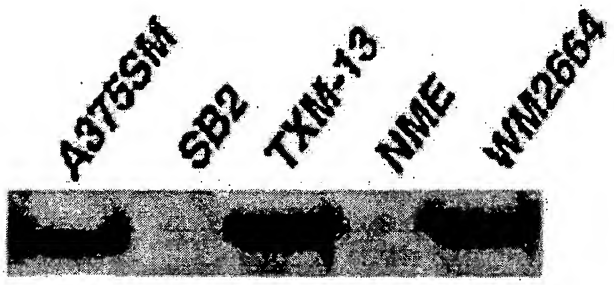

FIGURE 3

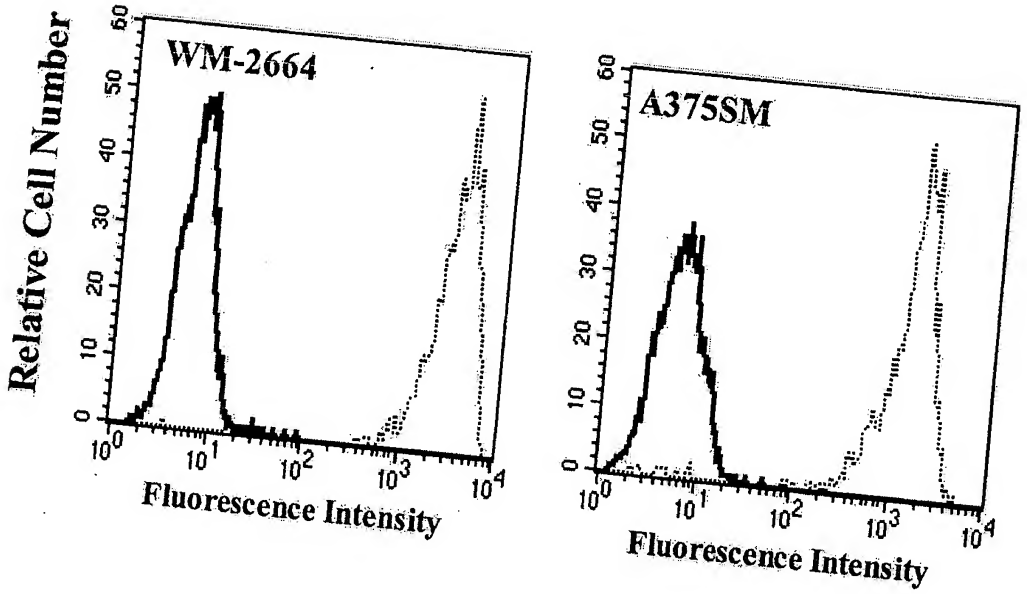
WM-2664
A375SM
Relative Cell Number
Fluorescence Intensity
Fluorescence Intensity
0
10
20
30
40
50
60
10^0
10^1
10^2
10^3
10^4

FIGURE 4

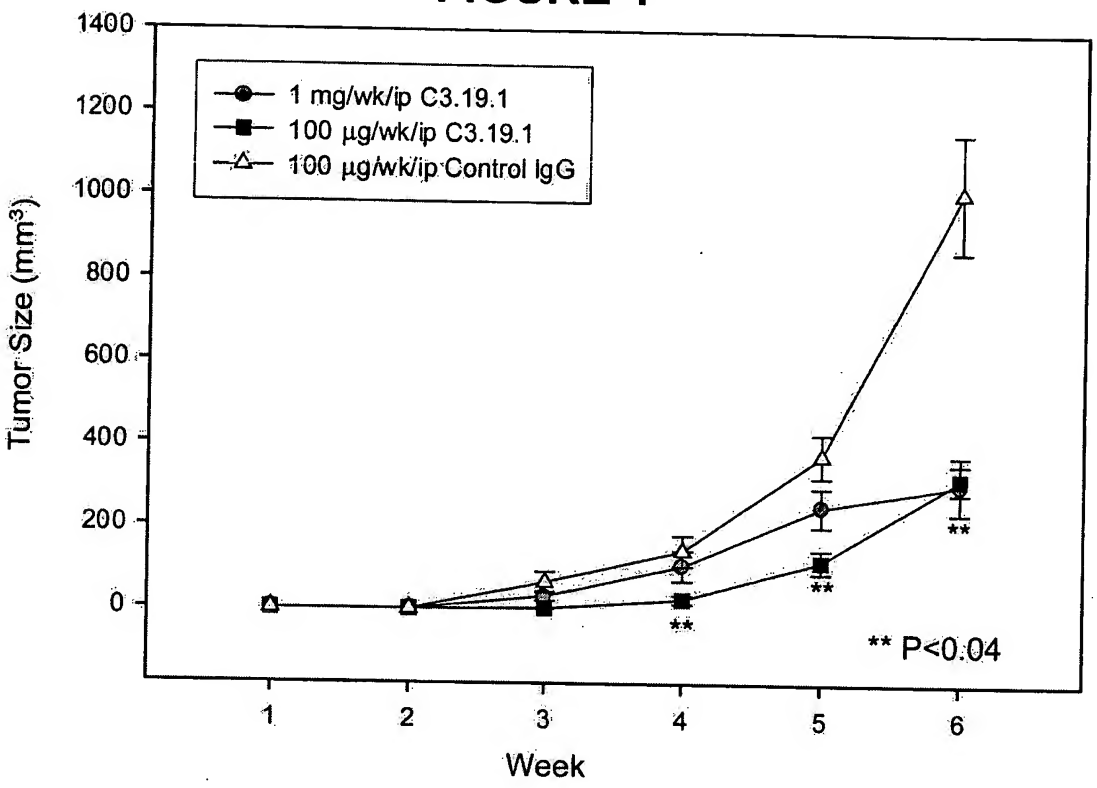
1400
1200
1000
800
600
400
200
0
Tumor Size (mm³)
1 mg/wk/ip C3.19.1
100 µg/wk/ip C3.19.1
100 µg/wk/ip Control IgG
** P<0.04
1
2
3
4
5
6
Week

FIGURE 5

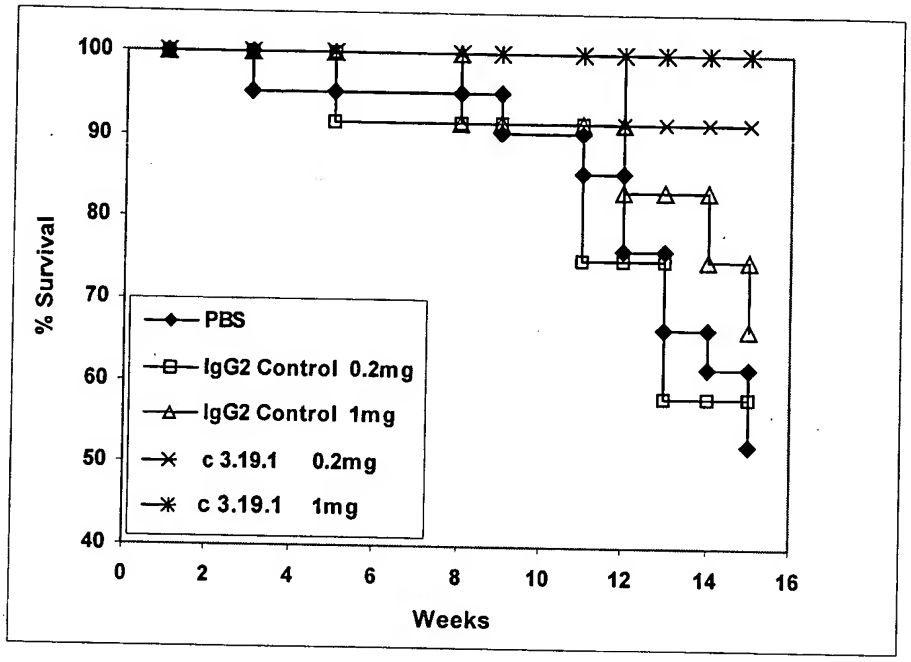
100
90
80
70
60
50
40
% Survival
0
2
4
6
8
10
12
14
16
Weeks
PBS
IgG2 Control 0.2mg
IgG2 Control 1mg
c 3.19.1 0.2mg
c 3.19.1 1mg

FIGURE 6

ANTI-MUC18 ANTIBODY C3.19.1

Nucleotide Sequence of heavy chain variable region

5′-
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGCTATATCTATTACACTTGGACCTCCAACTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTGGACACGTCCAAAAACCAGTTCTCCCTGAGGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTTTATTACTGTGCGAGAGATCAGGGGCAGTGGTTACTACCCGATGCTTTTGATATC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG 3′ (SEQ ID NO: 3)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYNPSLKSR
VTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWGQGTMVTVSS (SEQ ID
NO: 1)

Nucleotide Sequence of light chain variable region

5′-
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC
TGCAGGTCTAGTCAGAGCCTCCTGCGTAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAG
CCAGGACAGTCTCCACATCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGG
TTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAGCTCAACAAAGTCCGATCACCTTCGGCCAAGGGACACGACTGGAG
ATTAAAC 3′ (SEQ ID NO: 4)

Amino Acid Sequence of Light Chain Variable Region

DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRASGVPDR
FSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK (SEQ ID NO: 2)

FIGURE 7

ANTI-MUC18 ANTIBODY C6.11.13

Nucleotide Sequence of heavy chain variable region

5′-
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGGGGGAGATGGCTACAAGTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG-3′ (SEQ ID NO: 7)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGTLVTVSS (SEQ ID NO:
5)

Nucleotide Sequence of light chain variable region

5′
GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTAGCAACAACTTAGCCTGGTATCAGCAGAAACCTGGCCAGGCTCCC
AGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGT
CAGCAGTATAATAACTGGCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC 3′
(SEQ ID NO: 8)

Amino Acid Sequence of Light Chain Variable Region

EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG
SGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK (SEQ ID NO: 6)

FIGURE 8

ANTI-MUC18 ANTIBODY C3.10

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCAC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGCT CTGTGACCGC TGCGGACACG GCCCTTTATT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 11)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY IYYTWTTNYN
 61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT ALYYCARDQG QWLLPDAFDI WGQGTMVTVS
121 S (SEQ ID NO: 9)
```

Nucleotide Sequence of light chain variable region

```
  1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 61 ATCACTTGCC GGGCAAGTCA GAGCATTAGC AACTATTTAA ATTGGTATCA GCAGAAACCA
121 GGAAAAGCCC CTAAGCTCCT GATCTATGGT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG TCTGCAACCT
241 GAAGATTTTG CAACCTACTA CTGTCGACAG AGTTACAGTA CCCCTCCGGA GTGCAGTTTT
301 GGCCAGGGGA CCAAGCTGGA GATCAAAC (SEQ ID NO: 12)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIQMTQSPSS LSASVGDRVT ITCRASQSIS NYLNWYQQKP GKAPKLLIYG ASSLQSGVPS
 61 RFSGSGSGTD FTLTISSLQP EDFATYYCRQ SYSTPPECSF GQGTKLEIK (SEQ ID NO:
10)
```

FIGURE 9

ANTI-MUC18 ANTIBODY C3.22

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCACAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTGGTT ACTACTGGAC TTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTTCATCT ATTACAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAGTTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACTGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGAG
301 GGAGATGGCT TTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG (SEQ ID
NO: 15)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SGGYYWTWIR QHPGKGLEWI GFIYYSGSTY
 61 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAVYYCARE GDGFDYWGQG TLVTVSS (SEQ
ID NO: 13)
```

Nucleotide Sequence of light chain variable region

```
  1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAA TTCACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGCTCAC TTTCGGCGGA
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 16)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
 61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPLTFGG GTKVEIK (SEQ ID NO: 14)
```

FIGURE 10

ANTI-MUC18 ANTIBODY C3.27

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCTC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGTT CTGTGACCGC TGCGGACACG GCCGTTTACT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 19)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY IYYTWTSNYN
 61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT AVYYCARDQG QWLLPDAFDI WGQGTMVTVS
121 S (SEQ ID NO: 17)
```

Nucleotide Sequence of light chain variable region

```
  1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAG TTCACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGTGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 20)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
 61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPWTFGQ GTKVEIK (SEQ ID NO: 18)
```

FIGURE 11

ANTI-MUC18 ANTIBODY C3.45

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTTCAGC TGGTGCAGTC GGGAGCTGAG GTGAAGAAGC CTGGGGCCTC AGTGAAGGTC
 61 TCCTGCAAGG CTTCTGGTTA CACCTTTTTT AGCTATGGTT TCAGCTGGGT GCGACAGGCC
121 CCTGGACAAG GGCTTGAGTG GCTGGGATGG ATCAGCGCTT ACAATGGTAA CACAAACTAT
181 GCACAGAAGC TCCAGGGCAG AGTCACCATG ACCACAGACA CTTCCACGAG CACAGCCTAC
241 ATGGAGCTGA GGAGCCTGAG ATCTGACGAC ACGGCCGTGT ATTACTGTGC GAGAGAAACT
301 AAGGTTCGGG GAGTCCACTA CTACGGTATG GACGTCTGGG GCCAAGGGAC CACGGTCACC
361 GTCTCCTCAG (SEQ ID NO: 23)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLVQSGAE VKKPGASVKV SCKASGYTFF SYGFSWVRQA PGQGLEWLGW ISAYNGNTNY
 61 AQKLQGRVTM TTDTSTSTAY MELRSLRSDD TAVYYCARET KVRGVHYYGM DVWGQGTTVT
121 VSS (SEQ ID NO: 21)
```

Nucleotide Sequence of light chain variable region

```
  1 DIVMTQSPDS LAVSLGERAT IICKSSQSIL YSSNNKNYLG WYQQKPGQPP KLLIYWASTR
 61 ESGVPARFSG SGSGTDFTLT INSLQAEDVA VYYCQQYYST PRSFGQGTMV EIK (SEQ ID
NO: 24)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT CTCTGGGCGA GAGGGCCACC
 61 ATCATCTGCA AGTCCAGCCA GAGTATTTTA TACAGCTCCA ACAATAAGAA CTACTTAGGT
121 TGGTACCAGC AGAAACCAGG ACAGCCTCCT AAGCTGCTCA TTTACTGGGC ATCTACCCGG
181 GAATCCGGGG TCCCTGCCCG ATTCAGTGGC AGCGGGTCTG GGACAGATTT CACTCTCACC
241 ATCAACAGCC TGCAGGCTGA AGATGTGGCA GTTTATTACT GTCAGCAATA TTATAGTACT
301 CCTCGGTCGT TCGGCCAAGG GACCATGGTG GAAATCAAAC (SEQ ID NO: 22)
```

FIGURE 12

ANTI-MUC18 ANTIBODY C3.65

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCACAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAAC AGTGGTGGTT GCTACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTACATCT ATTCCAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAATTACC TTATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAACTCTAT GACTGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGAT
301 CGGGAAACAG CTGGTTTTGA CTACTGGGGC CAGGGAACCC TGGTCACCGT CTCCTCAG (SEQ
ID NO: 27)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLQESGPG LVKPSQTLSL TCTVSGGSIN SGGCYWSWIR QHPGKGLEWI GYIYSSGSTY
 61 YNPSLKSRIT LSVDTSKNQF SLKLNSMTAA DTAVYYCARD RETAGFDYWG QGTLVTVSS
(SEQ ID NO: 25)
```

Nucleotide Sequence of light chain variable region

```
  1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 61 ATCACTTGCC AGGCGAGTCA GGACATTAAC AACTATTTAA ATTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCTCCT GATCTACGAT GCATCCAATT TGGAAACAGG GGTCCCATCA
181 AGGTTCAGTG GAAGTGGATC TGGGACAGAT TTTACTTTCA CCATCAGCGG CCTGCAGCCT
241 GAGGATATTG CAACATATTA CTGTCAACAG TATGATACTC TCCCTCTCAC TTTCGGCGGC
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 28)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIQMTQSPSS LSASVGDRVT ITCQASQDIN NYLNWYQQKP GKAPKLLIYD ASNLETGVPS
 61 RFSGSGSGTD FTFTISGLQP EDIATYYCQQ YDTLPLTFGG GTKVEIK (SEQ ID NO: 26)
```

FIGURE 13

ANTI-MUC18 ANTIBODY C6.1

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGGTGGAGTC GGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC
 61 TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGCTATGCCA TGCACTGGGT CCGCCAGGCT
121 CCAGGCAAGG GGCTGGAGTG GGTGGCAGTT ATATCATATG ATGGAAGTAA TAAATACTAT
181 GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT
241 CTGCAAATGA ACAGCCTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGATCGATT
301 TTTGGAGTGG TTATCGACTA CGGTATGGAC GTCTGGGGCC AAGGGACCAC GGTCACCGTC
361 TCCTCAG (SEQ ID NO: 31)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV ISYDGSNKYY
 61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARSI FGVVIDYGMD VWGQGTTVTV
121 SS (SEQ ID NO: 29)
```

Nucleotide Sequence of light chain variable region

```
  1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
 61 ATCACTTGCC GGGCGAGTCA GGGCATTAGA AATTATTTAG CCTGGTATCA GCAGAATCCA
121 GGGAAAGTTC CTAAGCTCCT GATCTATGGT GCATCCACTT TGCAATCAGG GGTCCCATCT
181 CGGTTCAGTG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCAG CCTGCAGCCT
241 GAAGATGTTG CAACTTATTA CTGTCAAAAG TTTAGCAGTC CCCCATTCAC TTTCGGCCCT
301 GGGACCAAAG TGGATATCAG TC (SEQ ID NO: 32)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQNP GKVPKLLIYG ASTLQSGVPS
 61 RFSGSGSGTD FTLTISSLQP EDVATYYCQK FSSPPFTFGP GTKVDIS (SEQ ID NO: 30)
```

FIGURE 14

ANTI-MUC18 ANTIBODY C6.9

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGGAGCAGTC GGGGCCAGGA CTGGTGAAGC CTTCAGAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTACTT ACCACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAGGGGCCT GGAGTGGATT GGATACATCT ATTACAGTGG GAGCACCTAC
181 CACAACCCGT CCCTCAAGAG TCGAATTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACGGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGGG
301 GGAGATGGCT ACAGATACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG (SEQ ID
NO: 35)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLEQSGPG LVKPSETLSL TCTVSGGSIS SGTYHWSWIR QHPGRGLEWI GYIYYSGSTY
 61 HNPSLKSRIT ISVDTSKNQF SLKLSSVTAA DTAVYYCARG GDGYRYWGQG TLVTVSS (SEQ
ID NO: 33)
```

Nucleotide Sequence of light chain variable region

```
  1 GAAATAGTGA TGACGCAGTC TCCAGCCACC CTGTCTGTGT CTCCAGGGGA AAGAGCCACC
 61 CTCTCCTGCA GGGCCAGTCA GAGTATTAGC AACAACTTCG CCTGGTACCA GCAGAAACCT
121 GGCCAGGCTC CCAGGCTCCT CATCTTTGGT GCATCCACCA GGGCCACTGG TATCCCAGCC
181 AGGTTCAGTG GCAGTGGGTC TGGGACAGAA TTCACTCTCA CCATCAGCAG CCTACAGTCT
241 GAAGATTTTG CAGTTTATTA CTGTCAGCAG TATAATAACT GGCCTCGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 36)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 EIVMTQSPAT LSVSPGERAT LSCRASQSIS NNFAWYQQKP GQAPRLLIFG ASTRATGIPA
 61 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPRTFGQ GTKVEIK (SEQ ID NO: 34)
```

FIGURE 15

ANTI-MUC18 ANTIBODY C6.2

Nucleotide Sequence of heavy chain variable region

```
  1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CCTCGGAGAC CCTGTCCCTC
 61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT ACTTACTACT GGAGTTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGATAC ATCTATTACA CTGGGAACAC CTACTACAAC
181 CCCTCCCTCA AGAGTCGAGT CACCGTTTCA GTTGACACGT CCAAGAACCA GTTCTCCCTG
241 AAGCTGAACT CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGCGAG AGATCCAGGC
301 CAGTGGCTGG TCCCTGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CTCCGTCTCT
361 TCAG (SEQ ID NO: 39)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
  1 QVQLQESGPG LVKPSETLSL TCTVSGGSIS TYYWSWIRQP PGKGLEWIGY IYYTGNTYYN
 61 PSLKSRVTVS VDTSKNQFSL KLNSVTAADT AVYYCARDPG QWLVPDAFDI WGQGTMVSVS
121 S (SEQ ID NO: 37)
```

Nucleotide Sequence of light chain variable region

```
  1 GATATTGTGA TGACTCAGTC TCCACTCTCC CTGCCCGTCA TTCCTGGAGA GCCGGCCTCC
 61 ATCTCCTGCA GGTCTAGTCA GAGCCTCCTG CAGAGTAATG GAAACAACTA TTTGGATTGG
121 TACCTGCAGA AGCCAGGGCA GTCTCCACAG CTCCTGATCT ATTTGGGTTC TAATCGGGCC
181 TCCGGGGTCC CTGACAGGTT CAGTGGCAGT GGATCAGGCA CAGATTTTAC ACTGAAAATC
241 AGCAGAGTGG AGGCTGACGA TGTTGGGATT TATTACTGCA TGCAAGCTCT CCAAATTCCT
301 CTCACTTTCG GCGGAGGGAC CAAGGTGGAG ATCAAAC (SEQ ID NO: 40)
```

Amino Acid Sequence of Light Chain Variable Region

```
  1 DIVMTQSPLS LPVIPGEPAS ISCRSSQSLL QSNGNNYLDW YLQKPGQSPQ LLIYLGSNRA
 61 SGVPDRFSGS GSGTDFTLKI SRVEADDVGI YYCMQALQIP LTFGGGTKVE IK (SEQ ID
NO: 38)
```

FIGURE 16

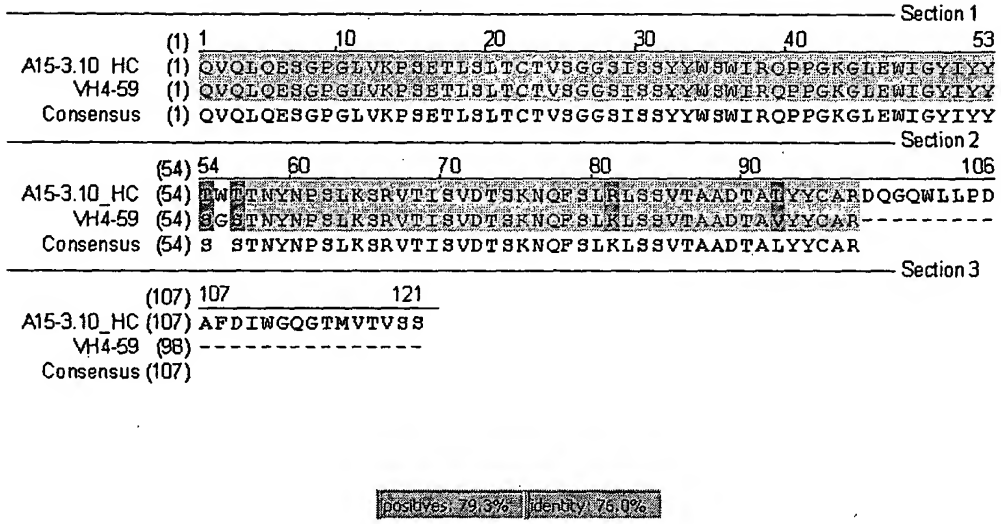
Section 1
(1) 1 10 20 30 40 53
A15-3.10_HC (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
VH4-59 (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Consensus (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Section 2
(54) 54 60 70 80 90 106
A15-3.10_HC (54) TWTTNYNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPD
VH4-59 (54) SGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---------
Consensus (54) S STNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCAR
Section 3
(107) 107 121
A15-3.10_HC (107) AFDIWGQGTMVTVSS
VH4-59 (98) ---------------
Consensus (107)
positives: 79.3%
identity: 76.0%

FIGURE 17

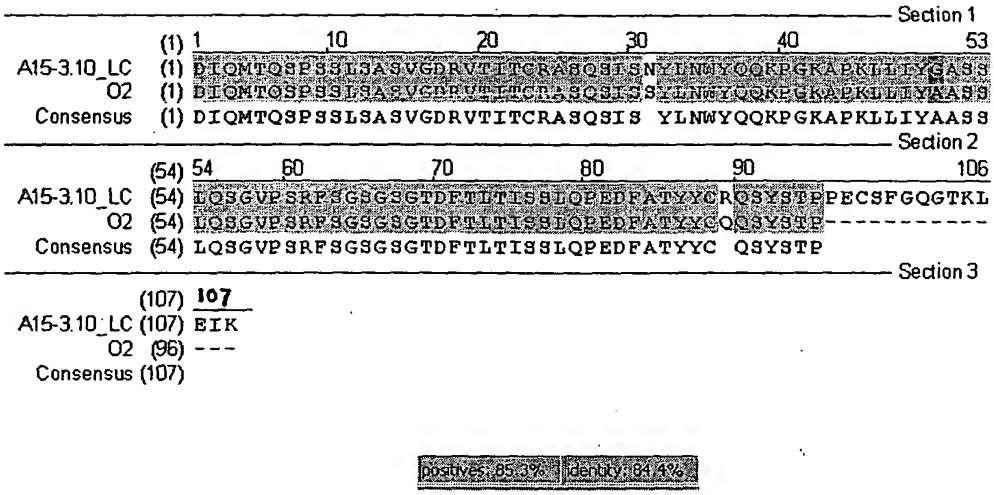
Section 1
(1) 1 10 20 30 40 53
A15-3.10_LC (1) DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASS
O2 (1) DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS
Consensus (1) DIQMTQSPSSLSASVGDRVTITCRASQSIS YLNWYQQKPGKAPKLLIYAASS
Section 2
(54) 54 60 70 80 90 106
A15-3.10_LC (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKL
O2 (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP----------
Consensus (54) LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC QSYSTP
Section 3
(107) 107
A15-3.10_LC (107) EIK
O2 (96) ---
Consensus (107)
positives: 85.3% identity: 84.4%

FIGURE 18

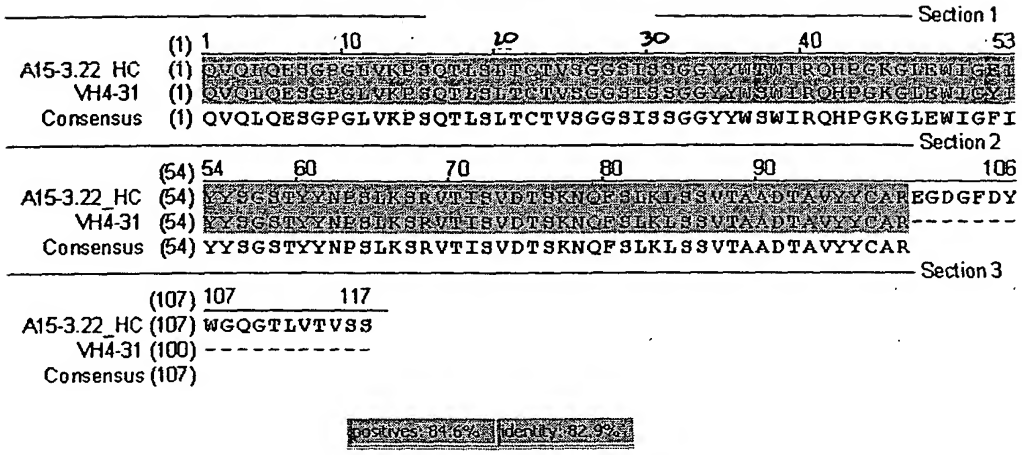
Section 1
(1) 1 10 20 30 40 53
A15-3.22_HC (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGFI
VH4-31 (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYI
Consensus (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGFI
Section 2
(54) 54 60 70 80 90 106
A15-3.22_HC (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGFDY
VH4-31 (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-------
Consensus (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
Section 3
(107) 107 117
A15-3.22_HC (107) WGQGTLVTVSS
VH4-31 (100) -----------
Consensus (107)
positives: 84.6%
identity: 82.9%

FIGURE 19

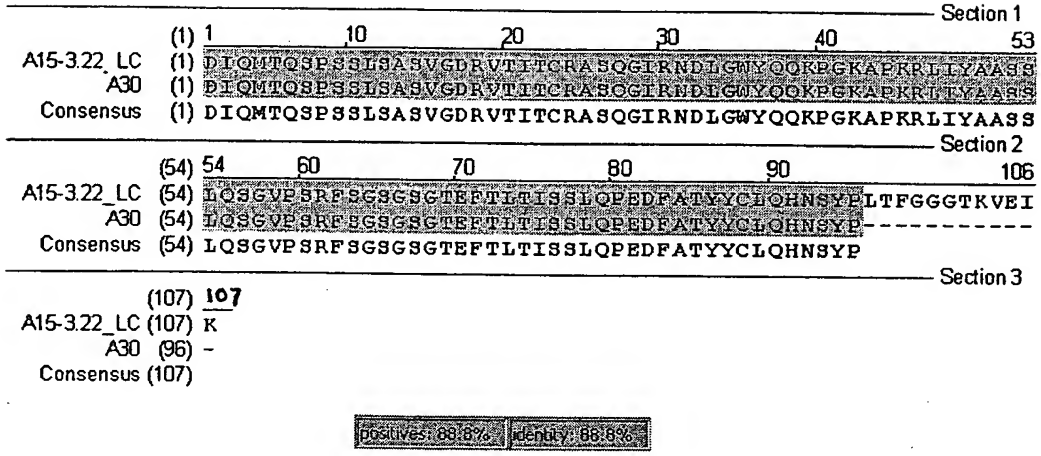
Section 1
(1) 1 10 20 30 40 53
A15-3.22_LC (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
A30 (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
Consensus (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
Section 2
(54) 54 60 70 80 90 106
A15-3.22_LC (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEI
A30 (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP----------
Consensus (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
Section 3
(107) 107
A15-3.22_LC (107) K
A30 (96) -
Consensus (107)
positives: 88.8%
identity: 88.8%

FIGURE 20

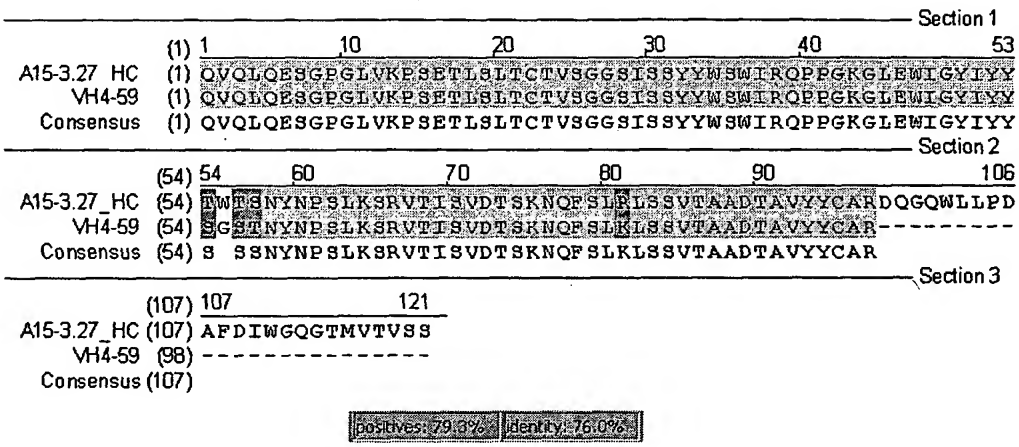
Section 1
(1) 1 10 20 30 40 53
A15-3.27_HC (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
VH4-59 (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Consensus (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Section 2
(54) 54 60 70 80 90 106
A15-3.27_HC (54) TWTSNYNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPD
VH4-59 (54) SGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---------
Consensus (54) S SSNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
Section 3
(107) 107 121
A15-3.27_HC (107) AFDIWGQGTMVTVSS
VH4-59 (98) ---------------
Consensus (107)
positives: 79.3%
identity: 76.0%

FIGURE 21

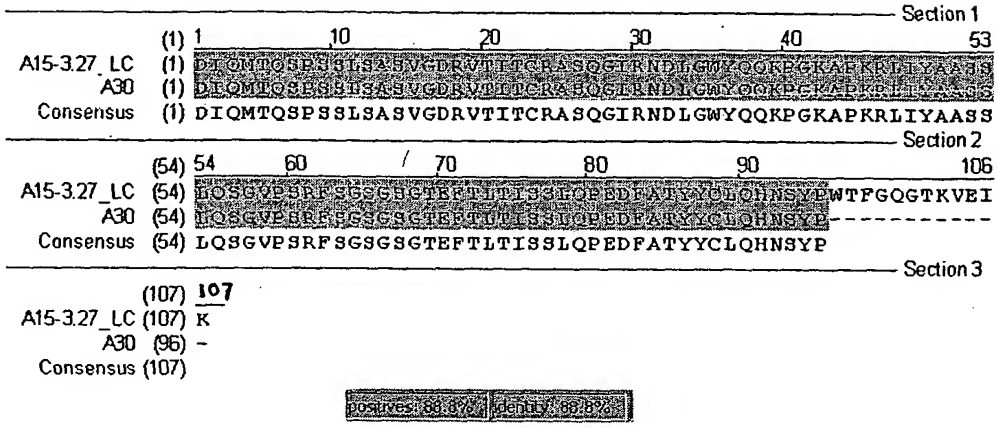
Section 1
(1) 1 10 20 30 40 53
A15-3.27_LC (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
A30 (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
Consensus (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS
Section 2
(54) 54 60 70 80 90 106
A15-3.27_LC (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEI
A30 (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP----------
Consensus (54) LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
Section 3
(107) 107
A15-3.27_LC (107) K
A30 (96) -
Consensus (107)
positives: 88.8% identity: 88.8%

FIGURE 22


Section 1
(1) 1 10 20 30 40 53
A15-3.45_HC (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFFSYGFSWVRQAPGQGLEWMGWISA
VH1-18 (1) QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
Consensus (1) QVQLVQSGAEVKKPGASVKVSCKASGYTF SYG SWVRQAPGQGLEWLGWISA
Section 2
(54) 54 60 70 80 90 106
A15-3.45_HC (54) YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARETKVRGVH
VH1-18 (54) YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--------
Consensus (54) YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
Section 3
(107) 107 123
A15-3.45_HC (107) YYGMDVWGQGTTVTVSS
VH1-18 (99) ----------
Consensus (107)
positives: 78.0% identity: 77.2%

FIGURE 23

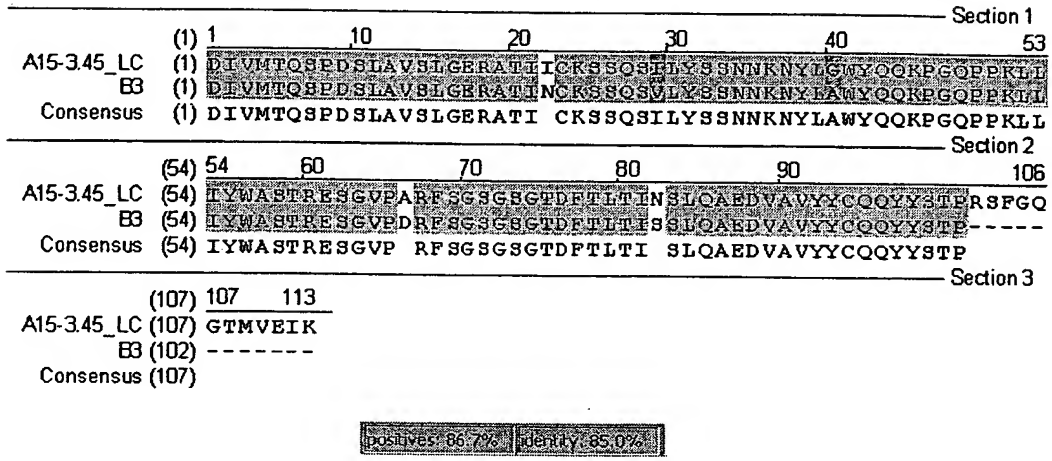
Section 1
(1) 1 10 20 30 40 53
A15-3.45_LC (1) DIVMTQSPDSLAVSLGERATIICKSSQSLLYSSNNKNYLGWYQQKPGQPPKLL
B3 (1) DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLL
Consensus (1) DIVMTQSPDSLAVSLGERATI CKSSQSILYSSNNKNYLAWYQQKPGQPPKLL
Section 2
(54) 54 60 70 80 90 106
A15-3.45_LC (54) IYWASTRESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQ
B3 (54) IYWASTRESGVPDRFSGSGSGTDFTITISSLQAEDVAVYYCQQYYSTP-----
Consensus (54) IYWASTRESGVP RFSGSGSGTDFTLTI SLQAEDVAVYYCQQYYSTP
Section 3
(107) 107 113
A15-3.45_LC (107) GTMVEIK
B3 (102) -------
Consensus (107)
positives: 86.7%
identity: 85.0%

FIGURE 24

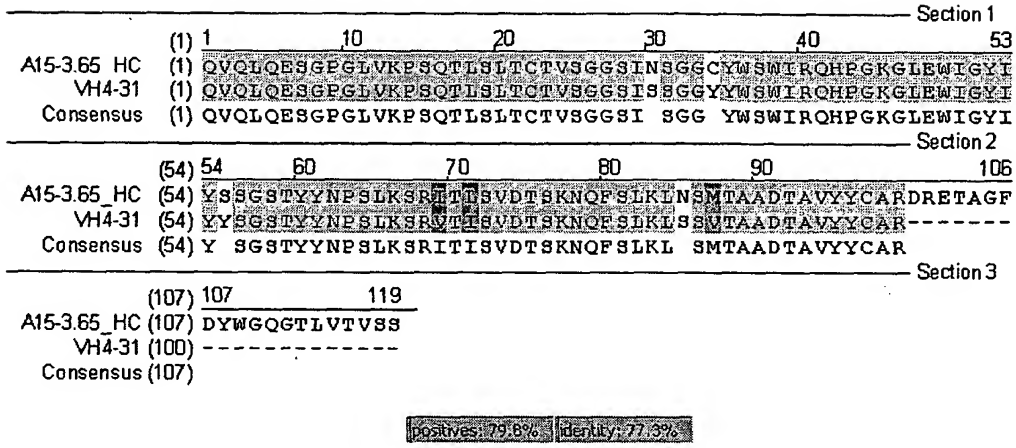
Section 1
(1) 1 10 20 30 40 53
A15-3.65_HC (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSINSGGCYWSWIRQHPGKGLEWIGYI
VH4-31 (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYI
Consensus (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSI SGG YWSWIRQHPGKGLEWIGYI
Section 2
(54) 54 60 70 80 90 106
A15-3.65_HC (54) YSSGSTYYNPSLKSRITISVDTSKNQFSLKLNSMTAADTAVYYCARDRETAGF
VH4-31 (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-------
Consensus (54) Y SGSTYYNPSLKSRITISVDTSKNQFSLKL SMTAADTAVYYCAR
Section 3
(107) 107 119
A15-3.65_HC (107) DYWGQGTLVTVSS
VH4-31 (100) -------------
Consensus (107)
positives: 79.6%
identity: 77.3%

FIGURE 25

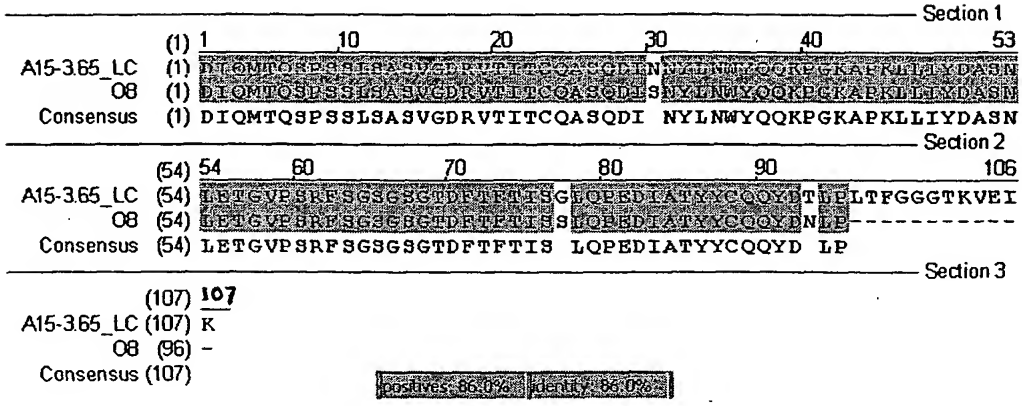
Section 1
(1) 1 10 20 30 40 53
A15-3.65_LC (1) DIQMTQSPSSLSASVGDRVTITCQASQDI NYLNWYQQKPGKAPKLLIYDASN
O8 (1) DIQMTQSPSSLSASVGDRVTITCQASQDI SNYLNWYQQKPGKAPKLLIYDASN
Consensus (1) DIQMTQSPSSLSASVGDRVTITCQASQDI NYLNWYQQKPGKAPKLLIYDASN
Section 2
(54) 54 60 70 80 90 106
A15-3.65_LC (54) LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVEI
O8 (54) LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP----------
Consensus (54) LETGVPSRFSGSGSGTDFTFTIS LQPEDIATYYCQQYD LP
Section 3
(107) 107
A15-3.65_LC (107) K
O8 (96) -
Consensus (107)
positives: 86.0% identity: 86.0%

FIGURE 26

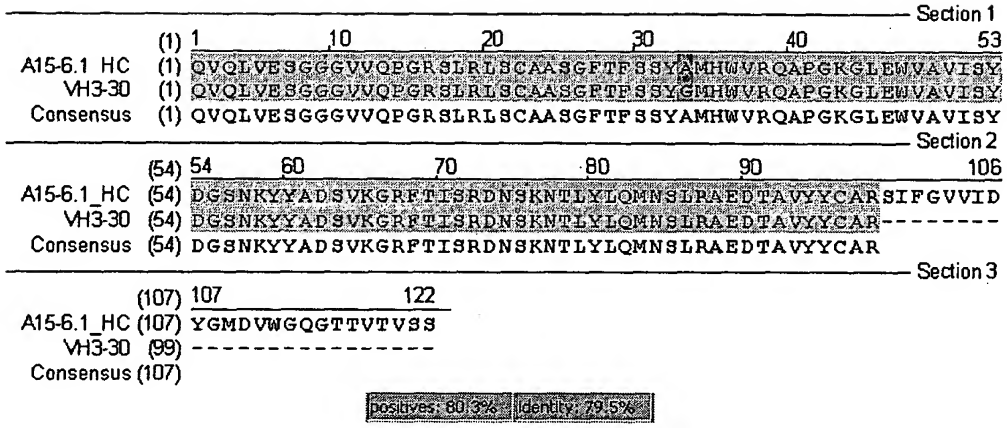
Section 1
(1) 1 10 20 30 40 53
A15-6.1_HC (1) QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISY
VH3-30 (1) QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISY
Consensus (1) QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISY
Section 2
(54) 54 60 70 80 90 106
A15-6.1_HC (54) DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSIFGVVID
VH3-30 (54) DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--------
Consensus (54) DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
Section 3
(107) 107 122
A15-6.1_HC (107) YGMDVWGQGTTVTVSS
VH3-30 (99) ----------
Consensus (107)
positives: 80.3%
identity: 79.5%

FIGURE 27

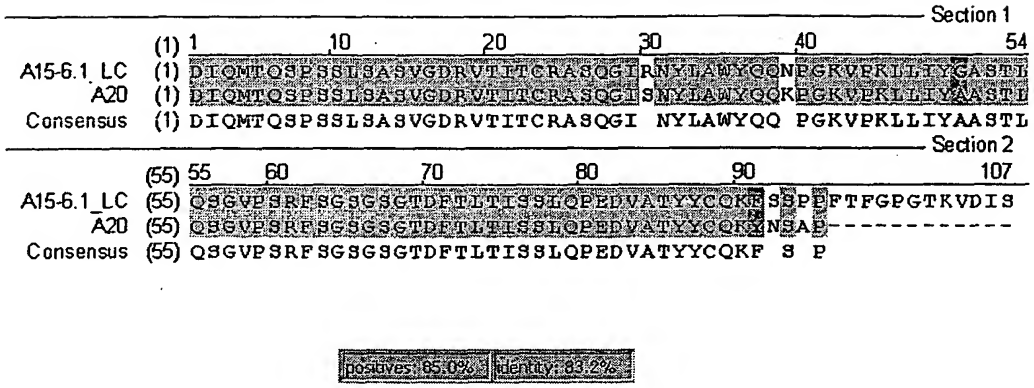
Section 1
(1) 1 10 20 30 40 54
A15-6.1_LC (1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTL
A20 (1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTL
Consensus (1) DIQMTQSPSSLSASVGDRVTITCRASQGI NYLAWYQQ PGKVPKLLIYAASTL
Section 2
(55) 55 60 70 80 90 107
A15-6.1_LC (55) QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDIS
A20 (55) QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQRYNSAP----------
Consensus (55) QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKF S P
positives: 85.0%
identity: 83.2%

FIGURE 28

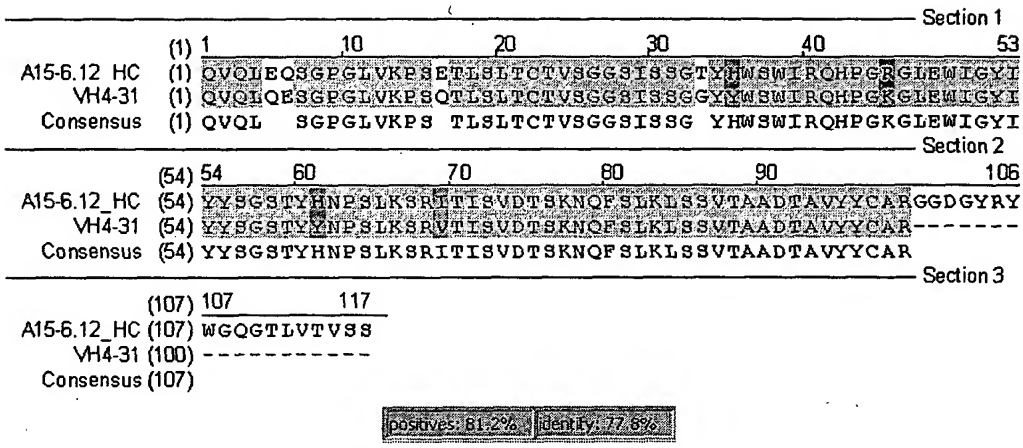
Section 1
(1) 1 10 20 30 40 53
A15-6.12_HC (1) QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYI
VH4-31 (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYI
Consensus (1) QVQL SGPGLVKPS TLSLTCTVSGGSISSG YHWSWIRQHPGKGLEWIGYI
Section 2
(54) 54 60 70 80 90 106
A15-6.12_HC (54) YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRY
VH4-31 (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-------
Consensus (54) YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR
Section 3
(107) 107 117
A15-6.12_HC (107) WGQGTLVTVSS
VH4-31 (100) ----------
Consensus (107)
positives: 81.2%
identity: 77.6%

FIGURE 29

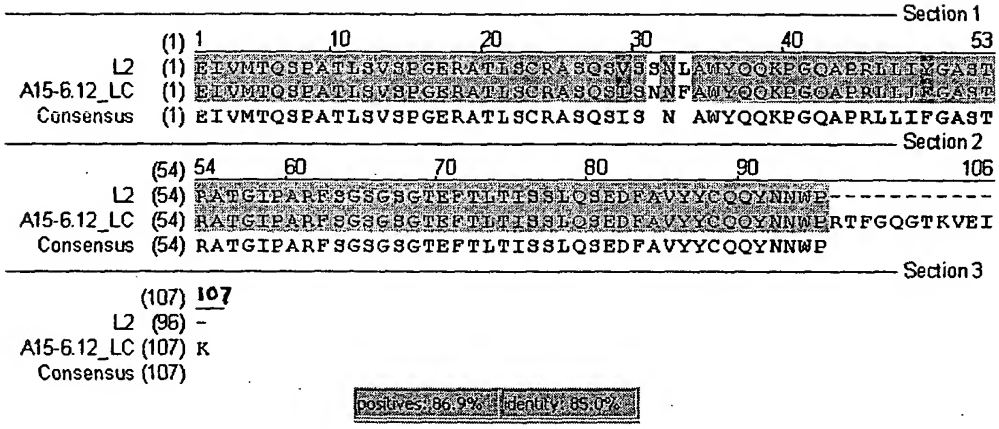
Section 1
(1) 1 10 20 30 40 53
L2 (1) EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAST
A15-6.12_LC (1) EIVMTQSPATLSVSPGERATLSCRASQSISSNNFAWYQQKPGQAPRLLIFGAST
Consensus (1) EIVMTQSPATLSVSPGERATLSCRASQSIS N AWYQQKPGQAPRLLIFGAST
Section 2
(54) 54 60 70 80 90 106
L2 (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP----------
A15-6.12_LC (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEI
Consensus (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
Section 3
(107) 107
L2 (96) -
A15-6.12_LC (107) K
Consensus (107)
positives: 86.9%
identity: 85.0%

FIGURE 30

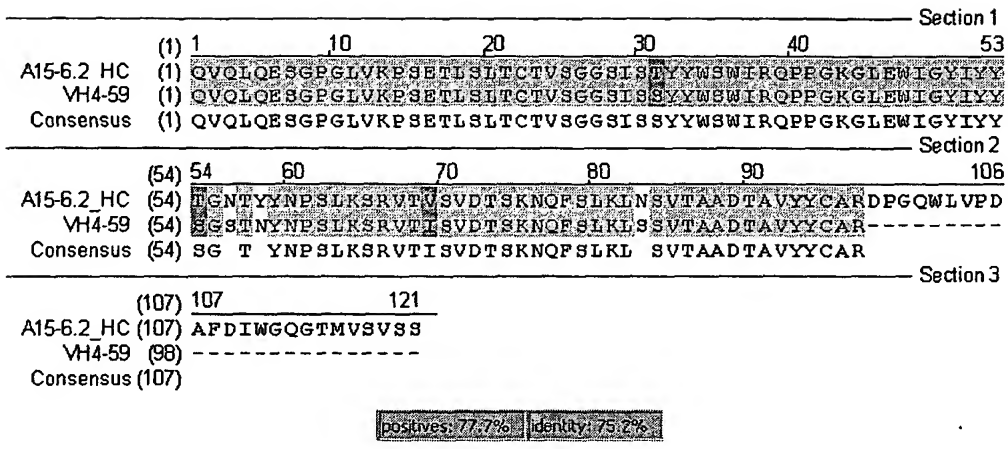
Section 1
(1) 1 10 20 30 40 53
A15-6.2_HC (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISDYYWSWIRQPPGKGLEWIGYIYY
VH4-59 (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Consensus (1) QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY
Section 2
(54) 54 60 70 80 90 106
A15-6.2_HC (54) TGNTYYNPSLKSRVTVSVDTSKNQFSLKLNSVTAADTAVYYCARDPGQWLVPD
VH4-59 (54) SGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR---------
Consensus (54) SG T YNPSLKSRVTISVDTSKNQFSLKL SVTAADTAVYYCAR
Section 3
(107) 107 121
A15-6.2_HC (107) AFDIWGQGTMVSVSS
VH4-59 (98) ---------------
Consensus (107)
positives: 77.7%
identity: 75.2%

FIGURE 31

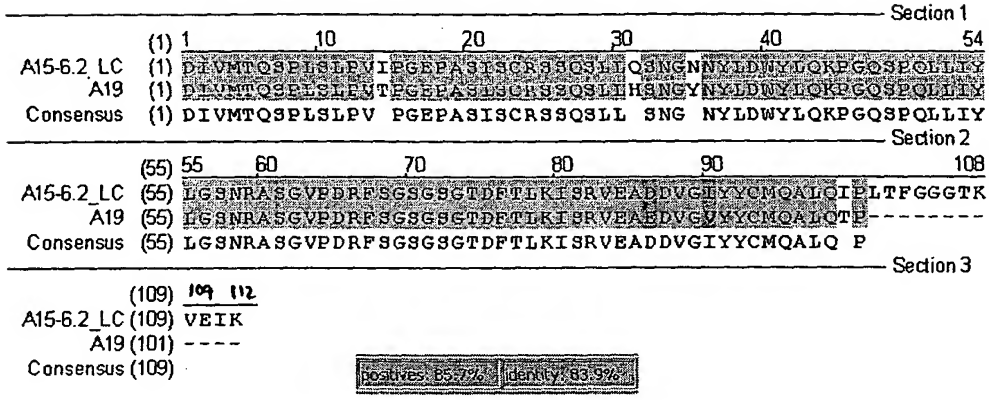
Section 1
(1) 1 10 20 30 40 54
A15-6.2_LC (1) DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIY
A19 (1) DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIY
Consensus (1) DIVMTQSPLSLPV PGEPASISCRSSQSLL SNG NYLDWYLQKPGQSPQLLIY
Section 2
(55) 55 60 70 80 90 108
A15-6.2_LC (55) LGSNRASGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTK
A19 (55) LGSNRASGVPDRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQTP--------
Consensus (55) LGSNRASGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQ P
Section 3
(109) 109 112
A15-6.2_LC (109) VEIK
A19 (101) ----
Consensus (109)
positives: 85.7% identity: 83.9%

FIGURE 32

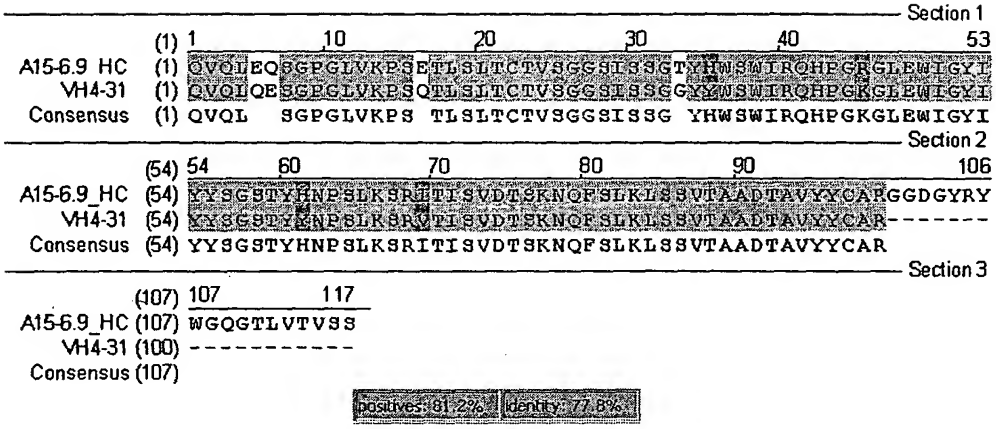
Section 1
(1) 1 10 20 30 40 53
A15-6.9_HC (1) QVQLEQSGPGLVKPSETLSLTCTVSGGSISSGTYHWSWIRQHPGRGLEWIGYI
VH4-31 (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYI
Consensus (1) QVQL SGPGLVKPS TLSLTCTVSGGSISSG YHWSWIRQHPGKGLEWIGYI
Section 2
(54) 54 60 70 80 90 106
A15-6.9_HC (54) YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYRY
VH4-31 (54) YYSGSTYENPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-------
Consensus (54) YYSGSTYHNPSLKSRITISVDTSKNQFSLKLSSVTAADTAVYYCAR
Section 3
(107) 107 117
A15-6.9_HC (107) WGQGTLVTVSS
VH4-31 (100) -----------
Consensus (107)
positives: 81.2%
identity: 77.8%

FIGURE 33

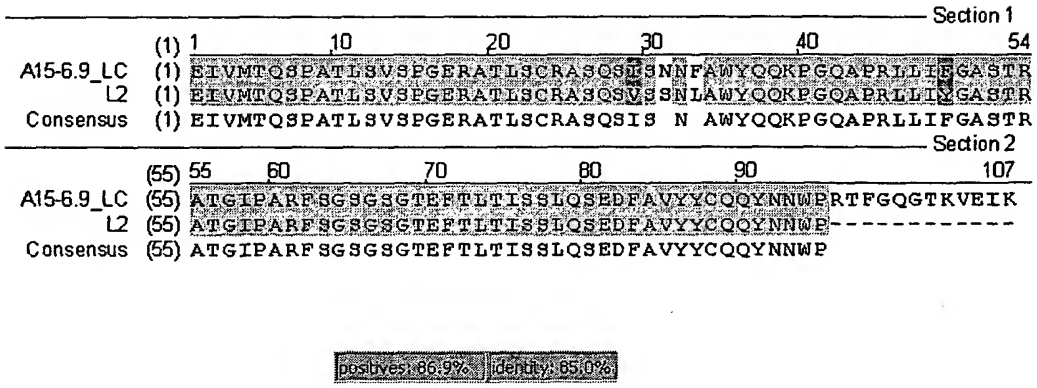
Section 1
(1) 1 10 20 30 40 54
A15-6.9_LC (1) EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTR
L2 (1) EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTR
Consensus (1) EIVMTQSPATLSVSPGERATLSCRASQSIS N AWYQQKPGQAPRLLIFGASTR
Section 2
(55) 55 60 70 80 90 107
A15-6.9_LC (55) ATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK
L2 (55) ATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP----------
Consensus (55) ATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
positives: 86.9% identity: 85.0%

FIGURE 34

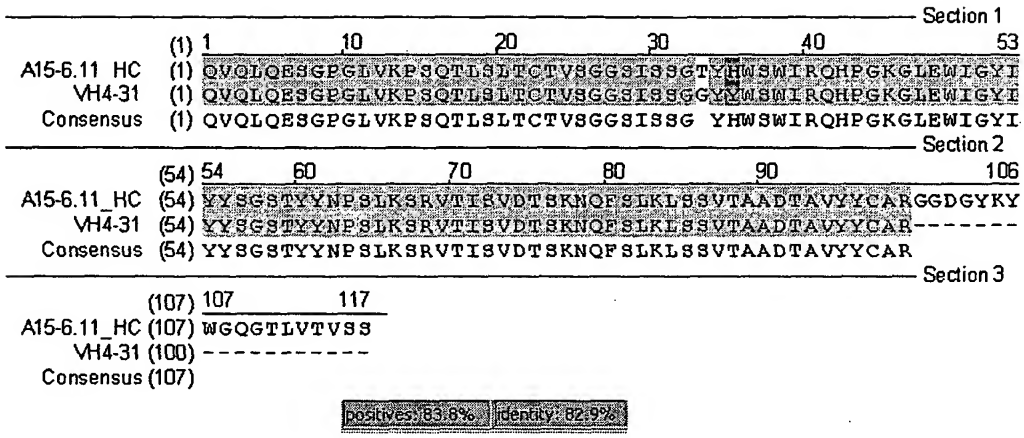
Section 1
(1) 1 10 20 30 40 53
A15-6.11_HC (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYI
VH4-31 (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYI
Consensus (1) QVQLQESGPGLVKPSQTLSLTCTVSGGSISSG YHWSWIRQHPGKGLEWIGYI
Section 2
(54) 54 60 70 80 90 106
A15-6.11_HC (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKY
VH4-31 (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-------
Consensus (54) YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
Section 3
(107) 107 117
A15-6.11_HC (107) WGQGTLVTVSS
VH4-31 (100) ----------
Consensus (107)
positives: 83.6%
identity: 82.9%

FIGURE 35

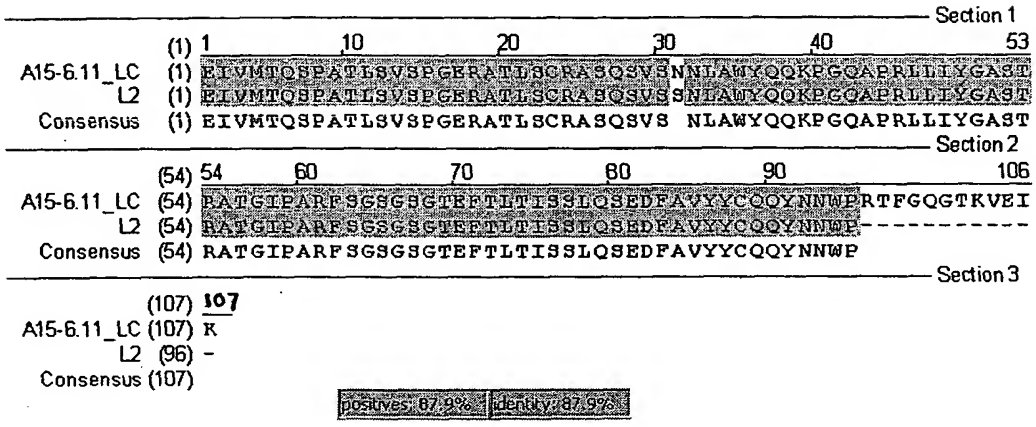
Section 1
(1) 1 10 20 30 40 53
A15-6.11_LC (1) EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGAST
L2 (1) EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAST
Consensus (1) EIVMTQSPATLSVSPGERATLSCRASQSVS NLAWYQQKPGQAPRLLIYGAST
Section 2
(54) 54 60 70 80 90 106
A15-6.11_LC (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEI
L2 (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP----------
Consensus (54) RATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
Section 3
(107) 107
A15-6.11_LC (107) K
L2 (96) -
Consensus (107)
positives: 87.9% identity: 87.9%

FIGURE 36

CLONE #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
A15-3.10	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.22	DP-65/4-31	0	GAGAGA	9	GGGAGATGG	-	-	-	-	-	JH4B	-4	CTTTGA
A15-3.27	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.45	DP-14/1-18	0	GAGAGA	6	AACTAA	D3-10	12	GGTTCGGGGAGT	2	CC	JH6B	-9	ACTACT
A15-3.65	DP-65/4-31	0	GAGAGA	8	TCGGGAAA	D6-13	8	CAGCTGGT	4	TTTT	JH5A	-11	GACTAC
A15-6.1	DP-49/3-30	3	GCGAGA	1	T	D3-3	18	CGATTTTTGGAGTGGTTA	3	TCG	JH6B	-12	ACTACG
A15-6.2	DP-71/4-59	0	GAGAGA	7	TCCAGGC	D6-19	11	CAGTGGCTGGT	5	CCCTG	JH3B	0	ATGCTT
A15-6.9	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG
A15-6.11	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	13	GAGATGGCTACAA	2	GT	JH1	-16	ACTGGG
A15-6.12	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG

CLONE	vk	#del	vk end	#n	N SEQ	Jk	# del	JK end
A15-3.10	02/012/DPK	0	CCCTCC	9	GGAGTGCAG	JK2	-7	TTTTGG
A15-3.22	A30	3	TTACCC	0	0	JK4	0	GCTCAC
A15-3.27	A30	3	TTACCC	0	0	JK1	0	GTGGAC
A15-3.45	B3/DPK24	1	TCCCTC	3	GGT	JK1	-5	CGTTCG
A15-3.65	08/018/DPK	1	TCCCTC	0	0	JK4	-2	TCACTTTC
A15-6.1	A20/DPK4	3	GTCCCC	0	0	JK3	0	ATTCAC
A15-6.2	A3/A19/DPK	1	TTCCTC	0	0	JK4	-2	TCACTTTC
A15-6.9	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.11	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.12	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT